

Manual of PATENT EXAMINING PROCEDURE

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WIPO Standard ST.25 (1998), Appendix 2, Table 3, provides that the amino acids should be represented using the following three-letter code with the first letter as a capital.

Table 3: List of Amino Acids

Symbol	Meaning
Ala	Alanine
Cys	Cysteine
Asp	Aspartic Acid
Glu	Glutamic Acid
Phe	Phenylalanine
Gly	Glycine
His	Histidine
Ile	Isoleucine
Lys	Lysine
Leu	Leucine
Met	Methionine
Asn	Asparagine
Pro	Proline
Gln	Glutamine
Arg	Arginine
Ser	Serine
Thr	Threonine
Val	Valine
Trp	Tryptophan
Tyr	Tyrosine
Asx	Asp or Asn
Glx	Glu or Gln
Xaa	unknown or other

WIPO Standard ST.25 (1998), Appendix 2, Table 4, provides that modified and unusual amino acids may

be represented as the corresponding unmodified amino acids in the sequence itself if the modified or unusual amino acid is one of those listed below and the modification is further described in the Feature section of the Sequence Listing. The codes from the list below may be used in the description (i.e., the specification and drawings, or in Sequence Listing) but these codes may not be used in the sequence itself.

Table 4: List of Modified and Unusual Amino Acids

Symbol	Meaning
Aad	2-Aminoadipic acid
bAad	3-Aminoadipic acid
bAla	beta-Alanine, beta-Aminopropionic acid
Abu	2-Aminobutyric acid
4Abu	4-Aminobutyric acid, piperidinic acid
Acp	6-Aminocaproic acid
Ahe	2-Aminoheptanoic acid
Aib	2-Aminoisobutyric acid
bAib	3-Aminoisobutyric acid
Apm	2-Aminopimelic acid
Dbu	2,4-Diaminobutyric acid
Des	Desmosine
Dpm	2,2' -Diaminopimelic acid
Dpr	2,3-Diaminopropionic acid
EtGly	N-Ethylglycine
EtAsn	N-Ethylasparagine
Hyl	Hydroxylysine
aHyl	allo-Hydroxylysine
3Hyp	3-Hydroxyproline
4Hyp	4-Hydroxyproline



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Appendix F Data Tables for Mod_Res Sequence Features

Appendix F provides a list (in alphabetical order) of additional modified residue (MOD_RES) **Sequence Features** that are displayed in the Features Screen when you have previously selected PRT as the **Sequence Type**, and MOD_RES from the listed sequence features in the pick list. After clicking on a sequence feature in the pick list, **MOD_RES** appears in the **Feature Name/Key** field (<221>), and the first **Add the following MOD-RES to the Other Information** field for MOD_RES (Table F-1) and second **Add the following MOD-RES to the Other Information** field for MOD_RES (Table F-2) sequence features appears. You can select from either one or both of the **Add the following MOD-RES to the Other Information** fields, and the data will appear in the **Other Information** field (<223>).

Table F-1: First Data Table for MOD_RES Sequence Features

Key	Description
(none)	blank space (default option)
ACETYLATION	N-terminal or other
AMIDATION	Generally at the c-terminal of a mature active peptide
BLOCKED	Undetermined n- or c-terminal blocking group
FORMYLATION	Of the n-terminal methionine
GAMMA-CARBOXYGLUTAMIC ACID HYDROXYLATION	Of asparagine, aspartic acid, proline or lysine
METHYLATION	Generally of lysine or arginine
PHOSPHORYLATION	Of serine, threonine, tyrosine, aspartic acid or histidine
PYRROLIDONE CARBOXYLIC ACID	N-terminal glutamate which has formed an internal cyclic lactam
SULFATATION	Generally of tyrosine

Table F-2: Second Data Table for MOD_RES Sequences

Symbol	Meaning
(none)	Blank space (default option)
Aad	2-Aminoadipic acid
bAad	3-Aminoadipic acid
bAla	beta-Alanine, beta-Aminopropionic acid
Abu	2-Aminobutyric acid
4Abu	4-Aminobutyric acid, piperidinic acid
Acp	6-Aminocaproic acid
Ahe	2-Aminoheptanoic acid
Aib	2-Aminoisobutyric acid
bAib	3-Aminoisobutyric acid
Apm	2-Aminopimelic acid
Dbu	2,4 Diaminobutyric acid
Des	Desmosine
Dpm	2,2'-Diaminopimelic acid